1/12

SEQUENCE LISTING

<110> National Agricultural Research Organization

<120> Nucleic acids encoding mirafiori lettuce viral proteins and utilization thereof.

<130> ARO-A0202P

<150> JP 2002-209805

<151> 2002-07-18

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 1514

<212> DNA

<213> mirafiori lettuce virus

<220>

<221> CDS

<222> (87).. (1400)

<400> 1

								2/	1 2	•						
gattattttt taaaaatata acaagctcat aagaaaacaa cttctccact caaaagtgaa 6														60		
tct	tcttttcaaa gaaaaacaaa gtcaca atg tca gga gta tac aag gtt tcc gga														113	
							Me	t Se	r Gl	y Va	1 Ty:	r Ly	s Va	l Se	r Gly	
	1 5															
att	cag	tct	atc	ttg	caa	aaa	gat	gtg	act	·tcc	gaa	gga	gaa	aca	gct	161
Ile	G1n	Ser	Ile	Leu	Gln	Lys	Asp	Val	Thr	Ser	Glu	Gly	G1u	Thr	Ala	
10					15					20					25	
-,-										-					20	
att	cta	att	tct	ctt	ggt	ctc	atg	aca	aaa	gaa	gag	aag	cct	gtt	cct	209
Ile	Leu	Ile	Ser	Leu	Gly	Leu	Met	Thr	Lys	Glu	Glu	Lys	Pro	Val	Pro	
				30					35					40		
gca	aaa	atg	gcc	atg	gtg	gca	tct	gca	aaa	gca	aac	tca	atc	atc	ttt	257
		Met														
1114	2,0	11100		1400	141	,,,,,	001		Lys	nia	non	UCI		110	THE	
			45					50					55			
														*		
gtt	tcg	gaa	gat	ggc	tct	ttg	tct	ttt	gaa	gct	cca	aaa	gaa	aca	gga	305
Val	Ser	Glu	Asp	Gly	Ser	Leu	Ser	Phe	Glu	Ala	Pro	Lys	Glu	Thr	Gly	
		60					65					70				
~ ~~	200	200	200	000	aac		000	000	ac a	acc	000	000	ato	400	at a	353
		agc														353
Glu	Thr	Ser	Lys	Pro	Gly	Glu	Lys	Lys	Glu	Glu	Lys	Lys	Val	Glu	Val	

gga	gtc	aag	ttt	cct	ttc	agc	gca	gcc	aaa	gta	aag	gag	cta	att	gaa	401
Gly	Val	Lys	Phe	Pro	Phe	Ser	Ala	Ala	Lys	Val	Lys	Glu	Leu	Ile	Glu	
90					95					100					105	
ggg	aaa	agt	ctt	act	ttg	gat	cag	gac	aaa	atc	caa	aaa	gtg	ctg	gaa	449
Gly	Lys	Ser	Leu	Thr	Leu	Asp	Gln	Asp	Lys	Ile	Gln	Lys	Val	Leu	Glu	
				110					115					120		
gaa	tat	gtt	aag	aat	ttg	cca	agg	act	gct	gag	act	tac	aaa	cca	aaa	497
G1u	Tyr	Val	Lys	Asn	Leu	Pro	Arg	Thr	Ala	Glu	Thr	Tyr	Lys	Pro	Lys	
			125					130					135			
gag	att	gag	atc	aaa	tgt	ttc	aag	ggt	gtt	gac	ttc	agt	ata	agc	agt	545
Glu	Ile	Glu	Ile	Lys	Cys	Phe	Lys	Gly	Val	Asp	Phe	Ser	Ile	Ser	Ser	
		140					145					150				
ttg	ctt	tct	tca	ggg	acc	aaa	atc	tta	gat	gct	att	ctt	tac	agt	act	593
Leu	Leu	Ser	Ser	Gly	Thr	Lys	Ile	Leu	Asp	Ala	Ile	Leu	Tyr	Ser	Thr	•
	155					160					165					
tac	aag	gat	tca	gca	gag	cac	aac	ttc	ata	ttt	gat	gtg	aaa	gtt	cta	641
Tyr	Lys	Asp	Ser	Ala	Glu	His	Asn	Phe	Ile	Phe	Asp	Val	Lys	Val	Leu	
170					175					180					185	

tct cct gat ttc atc gat agc aag tta ctc gtg aac aac atc gaa aca

Ser Pro Asp Phe Ile Asp Ser Lys Leu Leu Val Asn Asn Ile Glu Thr

				190					195					200		
ggc	aat	cga	gca	atc	aaa	gca	gct	ttc	tgt	ctt	gtt	tac	aat	caa	ggt	737
Gly	Asn	Arg	Ala	Ile	Lys	Ala	Ala	Phe	Cys	Leu	Val	Tyr	Asn	Gln	Gly	
			205					210					215			
gga	ttg	cca	tca	aag	acg	agt	gaa	gaa	cga	cca	cta	tct	aag	ttt	gta	785
Gly	Leu	Pro	Ser	Lys	Thr	Ser	Glu	Glu	Arg	Pro	Leu	Ser	Lys	Phe	Val	
		220					225					230				
aga	gaa	acg	ata	ttc	cgt	gag	aaa	gat	ctc	aaa	gct	aac	gag	tta	tgt	833
Arg	Glu	Thr	Ile	Phe	Arg	Glu	Lys	Asp	Leu	Lys	Ala	Asn	Glu	Leu	Cys	
	235					240					245					
gaa	tat	ctg	tca	tca	gca	gat	cct	tct	ttg	ttt	cca	agt	caa	gtc	ttt	881
Glu	Tyr	Leu	Ser	Ser	Ala	Asp	Pro	Ser	Leu	Phe	Pro	Ser	Gln	Val	Phe	
250					255					260					265	
ttg	aaa	atc	tca	ctt	gaa	aac	ctt	cct	act	gag	gtt	tca	tca	cgt	tgc	929
Leu	Lys	Ile	Ser	Leu	G1u	Asn	Leu	Pro	Thr	Glu	Val	Ser	Ser	Arg	Cys	
				270					275					280		
aag	atg	tcg	att	gcg	ggc	aac	aaa	gca	atg	aga	tat	gca	ctc	tta	gct	977

Lys Met Ser Ile Ala Gly Asn Lys Ala Met Arg Tyr Ala Leu Leu Ala

290

295

caa	aag	ttt	gac	aaa	gat	gaa	att	cca	gtt	cca	aca	gaa	gtg	aat	.cct	1025
Gln	Lys	Phe	Asp	Lys	Asp	Glu	Ile	Pro	Val	Pro	Thr	Glu	Val	Asn	Pro	
		300					305					310				
aca	act	agc	tca	gaa	tac	atg	cag	aaa	aag	gag	aaa	ata	gaa	aaa	gca	1073
Thr	Thr	Ser	Ser	Glu	Tyr	Met	Gln	Lys	Lys	Glu	Lys	Ile	Glu	Lys	Ala	
	315					320					325					
aaa	aag	ata	gtt	gat	gtt	cta	tgt	tct	ctt	gct	tct	gac	ttc	cag	gca	1121
Lys	Lys	Ile	Val	Asp	Val	Leu	Cys	Ser	Leu	Ala	Ser	Asp	Phe	G1n	Ala	
330					335					340					345	
caa	gtg	aaa	atg	cat	cct	ctc	tcc	cct	gag	aga	tca	tcg	agg	aag	aat	1169
G1n	Val	Lys	Met	His	Pro	Leu	Ser	Pro	Glu	Arg	Ser	Ser	Arg	Lys	Asn	
				350					355					360		
ttc	act	ctg	caa	ttg	act	tct	gca	att	gtt	act	tca	ctt	tcc	tac	aaa	1217
Phe	Thr	Leu	Gln	Leu	Thr	Ser	Ala	Ile	Val	Thr	Ser	Leu	Ser	Tyr	Lys	
			365					370					375			*
ggg	agg	tta	gac	atg	aga	aaa	gca	atc	gaa	gag	aaa	aag	ata	gag	gct	1265
Gly	Arg	Leu	Asp	Met	Arg	Lys	Ala	Ile	Glu	Glu	Lys	Lys	Ile	Glu	Ala	
		380					385					390				

ttc aaa aga gat gaa aat ata ttt gga agg tta aat gct ctt gga caa

Phe Lys Arg Asp Glu Asn Ile Phe Gly Arg Leu Asn Ala Leu Gly Gln

395 400 405

ccc acg ttt cct gtt ctg act aac gca gat gct gac ttt tct gaa ttg 1361
Pro Thr Phe Pro Val Leu Thr Asn Ala Asp Ala Asp Phe Ser Glu Leu
410 425

tca gtt gag gcc gtg aag aca gct tac gga aag aaa tga gggcagaatc 1410 Ser Val Glu Ala Val Lys Thr Ala Tyr Gly Lys Lys

430 435

ggagtgaata gtgaagaatg tggaattgtg gacagatttg cttttttccg cttatccttt 1470

gcgataggga gtatgtgaac tgatagtttt aataaaaaac tatc 1514

<210> 2

<211> 437

<212> PRT

<213> mirafiori lettuce virus

<400> 2

Met Ser Gly Val Tyr Lys Val Ser Gly Ile Gln Ser Ile Leu Gln Lys

1 5 10 15

Asp Val Thr Ser Glu Gly Glu Thr Ala Ile Leu Ile Ser Leu Gly Leu

20 25 30

Met Thr Lys Glu Glu Lys Pro Val Pro Ala Lys Met Ala Met Val Ala

		35					40					45			
Ser	Ala	Lys	Ala	Asn	Ser	Ile	Ile	Phe	Val	Ser	Glu	Asp	Gly	Ser	Leu
	50					55					60				
Ser	Phe	Glu	Ala	Pro	Lys	Glu	Thr	Gly	Glu	Thr	Ser	Lys	Pro	Gly	Glı
65					70					75					80
Lys	Lys	Glu	Glu	Lys	Lys	Val	Glu	Val	G1y	Val	Lys	Phe	Pro	Phe	Ser
				85					90					95	
Ala	Ala	Lys	Val	Lys	Glu	Leu	İle	Glu	Gly	Lys	Ser	Leu	Thr	Leu	Asp
			100					105					110		
Gln	Asp	Lys	Ile	Gln	Lys	Val	Leu	Glu	Glu	Tyr	Val	Lys	Asn	Leu	Pro
		115					120					125			
Arg	Thr	Ala	Glu	Thr	Tyr	Lys	Pro	Lys	Glu	Ile	Glu	Ile	Lys	Cys	Phe
	130					135					140				
Lys	Gly	Val	Asp	Phe	Ser	Ile	Ser	Ser	Leu	Leu	Ser	Ser	Gly	Thr	Lys
145					150					155					160
Ile	Leu	Asp	Ala	Île	Leu	Tyr	Ser	Thr	Tyr	Lys	Asp	Ser	Ala	Glu	His
				165					170					175	
Asn	Phe	Ile	Phe	Asp	Val	Lys	Val	Leu	Ser	Pro	Asp	Phe	Ile	Asp	Ser
			180					185					190		
Lys	Leu	Leu	Val	Asn	Asn	Ile	Glu	Thr	Gly	Asn	Arg	Ala	Ile	Lys	Ala
		195					200					205			
Ala	Phe	Cys	Leu	Val	Tyr	Asn	Gln	Gly	Gly	Leu	Pro	Ser	Lys	Thr	Ser
	210					215					220				
Glu	Glu	Arg	Pro	Leu	Ser	Lys	Phe	Val	Arg	Glu	Thr	<u>Į</u> le	Phe	Arg	Glu
225					230					235					240
we	Acr	Lou	Lvc	۸1۵	A an	C1	I	C	C1	Т	1	C	C	A 1 -	A

				245					250					255	
Pro	Ser	Leu	Phe	Pro	Ser	G1n	Val	Phe	Leu	Lys	Ile	Ser	Leu	Glu	Asn
			260					265					270		
Leu	Pro	Thr	Glu	Val	Ser	Ser	Arg	Cys	Lys	Met	Ser	Ile	Ala	Gly	Asn
		275					280					285			
Lys	Ala	Met	Arg	Tyr	Ala	Leu	Leu	Ala	Gln	Lys	Phe	Asp	Lys	Asp	Glu
	290					295					300				
Ile	Pro	Val	Pro	Thr	Glu	Val	Asn	Pro	Thr	Thr	Ser	Ser	Glu	Tyr	Met
305					310					315					320
G1n	Lys	Lys	Glu	Lys	Ile	Glu	Lys	Ala	Lys	Lys	Ile	Val	Asp	Val	Leu
				325					330					335	
Cys	Ser	Leu	Ala	Ser	Asp	Phe	Gln	Ala	Gln	Val	Lys	Met	His	Pro	Leu
			340					345			-		350		
Ser	Pro	Glu	Arg	Ser	Ser	Arg	Lys	Asn	Phe	Thr	Leu	Gln	Leu	Thr	Ser
		355					360					365			
Ala	Ile	Val	Thr	Ser	Leu	Ser	Tyr	Lys	Gly	Arg	Leu	Asp	Met	Arg	Lys
	370					375					380				
Ala	Ile	Glu	Glu	Lys	Lys	Ile	Glu	Ala	Phe	Lys	Arg	Asp	Glu	Asn	Ile
385					390					395					400
Phe	Gly	Arg	Leu	Asn	Ala	Leu	Gly	Gln	Pro	Thr	Phe	Pro	Val	Leu	Thr
				405					410					415	
Asn	Ala	Asp	Ala	Asp	Phe	Ser	Glu	Leu	Ser	Val	Glu	Ala	Val	Lys	Thr
			420					425					430		
Ala	Tyr	Gly	Lys	Lys											

<210> 3

⟨211⟩ 6

<212> PRT

<213> mirafiori lettuce virus

<400> 3

Glu Gly Glu Thr Ala Ile

1

5

<210> 4

⟨211⟩ 6

<212> PRT

<213> mirafiori lettuce virus

<400> 4

Leu Pro Thr Glu Val Ser

1

5

<210> 5

<211> 17

<212> DNA

<213> Artificial Sequence

<220> <223>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<220>

<221> modified_base

⟨222⟩ (6)

<223> i

<220>

<221> modified_base

<222> (12)

<223> i

<220>

<221> modified_base

<222> (15)

<223> i

<400> 5

garggngara cngcnat

17

<210> 6

<211> 17

<212> DNA

```
<213> Artificial Sequence
```

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

⟨220⟩

<221> modified_base

<222> (3)

<223> i

<220>

<221> modified_base

<222> (9)

<223> i

<220>

<221> modified_base

<222> (12)

<223> i

<220>

<221> modified_base

<222> (15)

<223> i

<400> 6

swnacytcng tnggnar